1. A system for assaying multiple nucleic acid molecules in one or more biological samples having one or more nucleic acid targets per sample comprising:

a plurality of nucleic acid probes, wherein each nucleic acid of the plurality is different from other nucleic acids in the plurality, and

a plurality of intermediary nucleic acids, wherein each intermediary nucleic acid comprises a first region and a second region, wherein each intermediary nucleic acid is different from other intermediary nucleic acids in the plurality of intermediary nucleic acids by comprising a different first region, wherein the first region of each intermediary nucleic acid is complementary to a different nucleic acid probe of the plurality of nucleic acid probes, and wherein the second region of each intermediary nucleic acid is complementary to a potential target nucleic acid in a sample, wherein each probe of the plurality of nucleic acid probes and each second region of each intermediary nucleic acid comprises unstructured nucleotides, such that the second region of each intermediary nucleic acid has a reduced ability to form a stable duplex with a nucleic acid probe having regions of complementarity, wherein the second region of each intermediary nucleic acid forms a stable duplex with a complementary target nucleic acid, and wherein each nucleic acid probe forms a stable duplex with a complementary first region of an intermediary nucleic acid

2. The system of claim 1, wherein the nucleic acid probes comprising modified and unmodified nucleotides and the second region of intermediary nucleic acids comprising modified nucleotides comprise complementary nucleotides that have a

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reduced ability to form base pairs with each other, wherein the modified nucleotides form base pairs with unmodified nucleotides.

3. The system of claim 1, wherein the modified nucleotides comprise A' and T' wherein A' and T' have a reduced ability to form a base pair, wherein A' forms a base pair with T*, and wherein T' forms a base pair with A*.

4. The system of claim 3, wherein A' is 2-aminoadenosine, wherein T' is 2-thiothymidine, wherein A* is adenosine and wherein T* is thymidine.

5. The system of claim 1, wherein the modified nucleotides comprise G' and C' wherein G' and C' have a reduced ability to form a base pair, wherein G' forms a base pair with C*, and wherein C' forms a base pair with G*.

6. The system of claim 3, wherein G' is inosine, wherein C' is pyrrolopyrimidine, wherein G* is guanosine and wherein C* is cytosine.

7. The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe corresponds to a known location in the array pattern.

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8. The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe is associated with a known bead particle.

9. The system of claim 1, wherein the plurality of nucleic acid probes is fixed on a substrate in an array pattern, wherein a sequence of a nucleic acid probe is associated with a defined tag moiety wherein the tag is detectable by mass electrophoretic mobility or optical property.

10. A method of assaying target nucleic acid molecules by tagging and sorting the target molecules, comprising the steps of:

a) providing a first plurality of nucleic acids, wherein each nucleic acid of the first plurality is different from other nucleic acids in the first plurality;

b) providing a second plurality of nucleic acids , wherein each second nucleic acid of the second plurality comprises a first region and a second region, wherein each first region of each second nucleic acid has a different sequence from other first regions of other nucleic acids in the second plurality, wherein the first region of each second nucleic acid is complementary to a different first nucleic acid of the first plurality, wherein at least one second region of the second nucleic acids in the second plurality is complementary to a target nucleic acid in a biological samples, wherein each first nucleic acid of the first plurality and each second region of each second nucleic acid of the second plurality comprise unstructured nucleotides such that the second region of each second nucleic acid has a reduced ability to hybridize to a first

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probe of the first plurality having a complementary sequence without reducing the ability of the second region of each second nucleic acid to hybridize to a complementary nucleic acid molecule in a biological sample;

c) providing a biological sample containing nucleic acids to be analyzed;

d) contacting the biological sample with the second plurality of probes under conditions that permit hybridization of complementary sequences between the nucleic acid molecules in the sample and the second region of a second nucleic acids of the second plurality;

e) contacting the second plurality of probes with the first plurality of probes under conditions that permit hybridization of complementary sequences between the first region of a second probe of the second plurality and the first probes in the first plurality

f) detecting nucleic acids in the biological sample that have hybridized to a nucleic acid of the second plurality; and

g) determining the sequence of the nucleic acid in the biological sample that has hybridized to a nucleic acid of the second plurality.

11. The method of claim 10, wherein the steps of (d) and (e) are performed simultaneously.

12. The method of claim 10, wherein after step (e), unhybridized nucleic acids are removed.

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13. The method of claim 10, wherein the step of detecting further comprises detecting by measuring light emission.

14. The method of claim 10, wherein the step of contacting the biological sample with the second plurality of probes further comprises labeling the probes that having hybridized with a nucleic acid in the sample with a detectable label.

15. A kit comprising an array apparatus comprising a plurality of nucleic acid probes on a substrate in an array pattern such that a sequence of a nucleic acid probe corresponds to a known location in the array pattern, wherein each nucleic acid of the plurality is different from other nucleic acids in the plurality, and

a plurality of intermediary nucleic acids, wherein each intermediary nucleic acid comprises a first region and a second region, wherein each intermediary nucleic acid is different from other intermediary nucleic acids in the plurality of intermediary nucleic acids by comprising a different first region, wherein the first region of each intermediary nucleic acid is complementary to a different nucleic acid probe of the plurality of nucleic acid probes, and wherein the second region of each intermediary nucleic acid is complementary to a potential target nucleic acid in a sample, wherein each probe of the plurality of nucleic acid probes and each second region of each intermediary nucleic acid comprises unstructured nucleotides, such that the second region of each intermediary nucleic acid has a reduced ability to form a stable duplex with a nucleic acid probe having regions of complementarity, wherein the second region of each intermediary nucleic acid forms a stable duplex with a complementary

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target nucleic acid, and wherein each nucleic acid probe forms a stable duplex with a complementary first region of an intermediary nucleic acid.

16. The kit of claim 15, wherein the unstructured nucleotides are selected from the group consisting of: 2-aminoadenosine, 2-thiothymidine, inosine, and pyrrolopyrimidine.

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